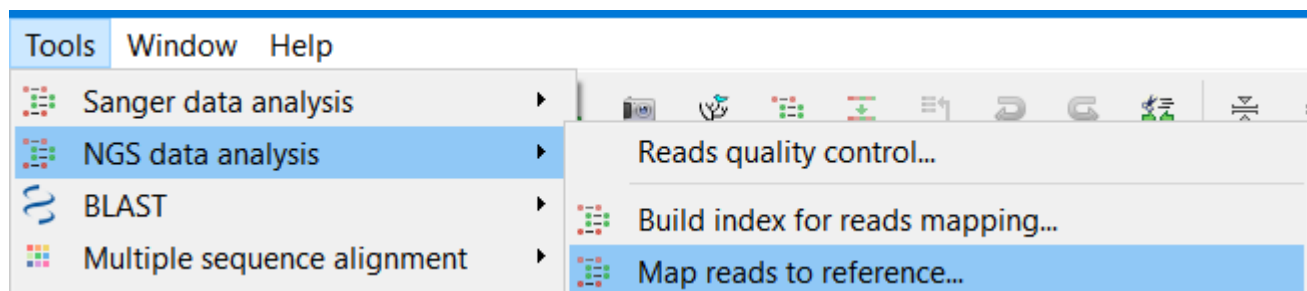


# UGENE Genome Aligner

The [UGENE Genome Aligner](#) is a fast short read aligner. It aligns DNA sequences of various lengths to the reference genome with configurable mismatch rate.

It is available from the *Tools* *NGS data analysis* submenu of the main menu.



Select the *Map reads to reference* item to align short reads to a DNA sequence or *Build index for reads mapping* item to build an index for a DNA sequence which can be used to optimize aligning short reads to the sequence.

- [Building Index for UGENE Genome Aligner](#)
- [Converting UGENE Assembly Database to SAM Format](#)
- [Map NGS Reads with UGENE Genome Aligner](#)